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Supplementary Information for

A global phylogeny of turtles reveals a burst of climate-associated diversification on continental margins

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Supplementary Results and Discussion

The phylogeny that we recovered (Fig. S1) confirms many evolutionary relationships among the major lineages of turtles (see Results and Discussion). Within families, the tree that we recover is generally congruent with earlier work, although several novel relationships deserve mention. The few cases of genus-level non-monophyly that we recovered are mostly centered within the highly speciose Deirochelyinae subfamily of Emydidae (Fig. S1). This clade contains several genera that appear to have diversified extraordinarily rapidly and have long presented a challenge for accurate phylogenetic resolution (1–4). An earlier analysis of the deirochelyine genus *Pseudemys* indicated that results were sensitive to the particular individuals used in the analysis and uncovered pervasive uncertainty in this part of the tree, likely owing to its recent and rapid diversification (3). We provisionally view our phylogenetic results for the deirochelyine genera *Trachemys*, *Graptemys*, and *Pseudemys* in this same way, and suspect that they are likely influenced by stochastic error and coalescent sorting associated with very short branches. Targeted analyses that focus specifically on these clades and employ widespread within-species sampling have had more success clarifying these challenging nodes (e.g., 32).

Outside of Emydidae, we identified two additional cases of genus level non-monophyly. Within the tortoises (Testudinidae), we found that the monotypic *Chersina angulata* renders *Homopus* paraphyletic, confirming the results of Hofmeyr et al (5). We recommend combining these genera into *Chersina*, which has priority, as this would address the issue of non-monophyly and avert the use of a monotypic name that conveys no information about evolutionary relatedness (6). Similarly, we confirmed that the monotypic *Stigmochelys pardalis* is sister to *Psammobates*, within which it was formerly included. Although both *Stigmochelys* and *Psammobates* were reconstructed as monophyletic, we recommend returning *S. pardalis* to *Psammobates* to convey their close evolutionary relatedness. Finally, our analysis rendered the South American sideneck genus *Mesoclemmys* paraphyletic with respect to *Phrynos* by the placement of the enigmatic, critically endangered *M. hogei* as sister group to the remaining species of *Mesoclemmys* + *Phrynos*. The interrelationships of these species continue to be one of the most challenging phylogenetic problems in the family Chelidae. We make no taxonomic recommendations, but point out that the combination of management of some of the most

endangered turtles on earth (*M. hogei*, *M. dahli*) and taxonomic uncertainty indicate that further work is needed to clarify these relationships.

Within the family Geoemydidae, previous studies have recovered the genus *Rhinoclemmys* as sister to the remaining members of the family (7–11). *Rhinoclemmys* is the only member of the family native to the Americas, suggesting that it may have diverged early in the history of Geoemydidae. By contrast, we recover three reciprocally monophyletic groups within the family, including 1) a clade containing several Indian and Southeast Asian genera (*Siebenrockiella*, *Orlitia*, *Malayemys*, *Geoclemys*, *Morenia*, *Pangshura*, and *Batagur*) sister to 2) *Rhinoclemmys* and 3) a clade containing the remaining 10 geoemydid genera. Although the branch lengths supporting these relationships are short, they receive high support (posterior probabilities all > 0.95, Fig. S1), and suggest a dramatically different early biogeographic history for the family. To our knowledge, this is a novel hypothesis and clearly deserves further scrutiny. These Indian and Southeast Asian genera have been sampled in previous phylogenetic studies relatively rarely, and the most recent and large scale analyses do not include the necessary taxa to evaluate this hypothesis (12, 13). The most salient difference between our analysis and all previous analyses that recover *Rhinoclemmys* as sister to the Asian taxa is that a large fraction of those datasets focused on data collected from a single locus (the mitochondrion), whereas we sample only nuclear DNA. This difference appears to explain at least some other conflicts among alternative analyses of turtle phylogeny. For example, analyses based on full mitochondrial genomes (14, 15) recovered a different view for the phylogenetic position of sea turtles than most other analyses (8, 12, 13, 16, 17). Adding genomic data from *Siebenrockiella*, *Orlitia*, *Malayemys*, *Geoclemys*, *Morenia*, *Pangshura*, and/or *Batagur* to existing genome scale datasets would allow for a strong test of this hypothesis.

We were able to obtain samples of at least two individuals for 230 species (82% of species in the tree, and 66% of all turtles). Among these, we found that 183 (80%) were monophyletic in the majority rule consensus tree. Again, the largest departures from species monophyly occurred within the Deirochelyinae subfamily of Emydidae, and were mostly located in the most species rich genera in that clade (including *Graptemys*, *Pseudemys*, and *Trachemys*). Outside of the Emydidae, most mismatches between species level taxonomy and estimated

phylogeny occurred within the mud and musk turtles (Kinosternidae) and tortoises (Testudinidae).

Many of these cases represent splits that have been recognized in the last few decades, often based on molecular assessments of one or a few genes. These highlight areas where additional taxon and data sampling are critical before further taxonomic revisions are attempted.

Our analysis lacks data from 69 of the currently recognized extant species, mostly centered in the Pleurodira, a clade which has been less intensively studied than the Cryptodira, yet contains a large amount of diversity. The tree is also missing several of the softshell turtles (Trionychidae), which is one of the most ancient lineages of crown group turtles and contains many critically endangered species. The phylogenetic placement for some of these missing taxa is reasonably well understood, while others present a real source of uncertainty. For example, we were not able to collect data for the flatback sea turtle, *Natator depressus*, although it is known to be a member of the extant marine turtles (family Cheloniidae), likely sister to *Chelonia* (18–20). Likewise, we were unable to obtain data for the large softshell turtle *Rafetus euphraticus*. It is almost certainly sister to the congeneric species *Rafetus swinhoei* (of which only three remaining individuals are known in the world and for which we do have data). Others are less certain. For example, the chelid turtle *Pseudemydura umbrina* is one of the most threatened turtle species in the world. It is restricted to a small area of western Australia that has experienced extensive habitat declines. The species is most likely sister to the clade that contains all other Australian chelids, although some uncertainty remains (21–24).

Supplementary Figure Legends

Figure S1a. Majority rule consensus phylogram estimated from Bayesian phylogenetic analysis of the concatenated partitioned dataset. Dots on the nodes indicate posterior probability: black > 0.95; gray 0.75 - 0.95; white < 0.75.

Figure S1b. continued from figure S1a.

Figure S1c. continued from figure S1b.

Figure S1d. continued from figure S1c.

Figure S1e. continued from figure S1d.

Figure S2. Results from best fitting geographic diversification rate model in Table 2. A) Ancestral range estimates reconstruct nearly all transitions to coastal areas occurring after the Eocene-Oligocene (dashed line) when these areas would have been exposed. B) Estimates of net diversification and speciation indicate higher rates in coastal than inland areas. Results are qualitatively similar to the model averaged analysis (Fig. 3).

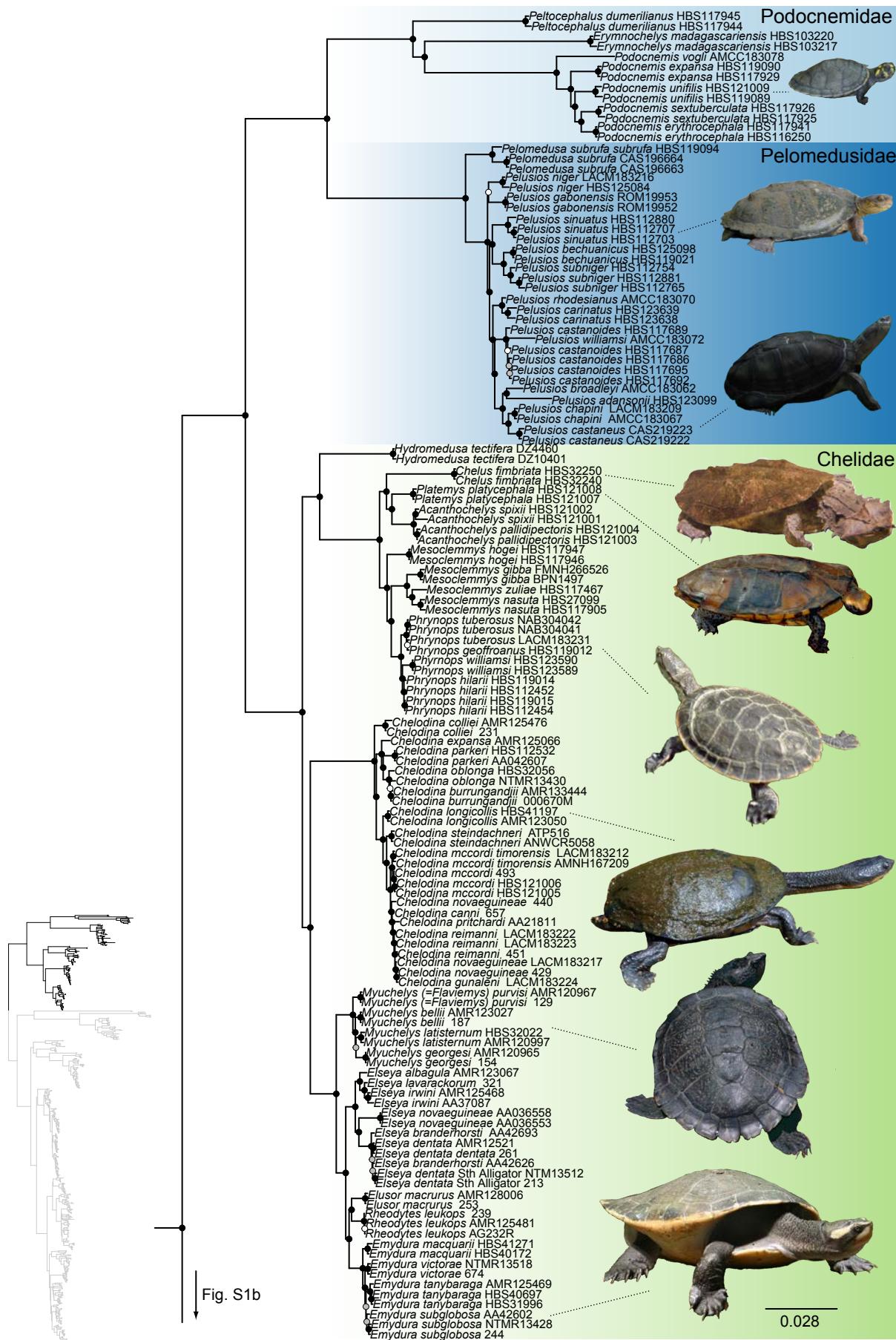
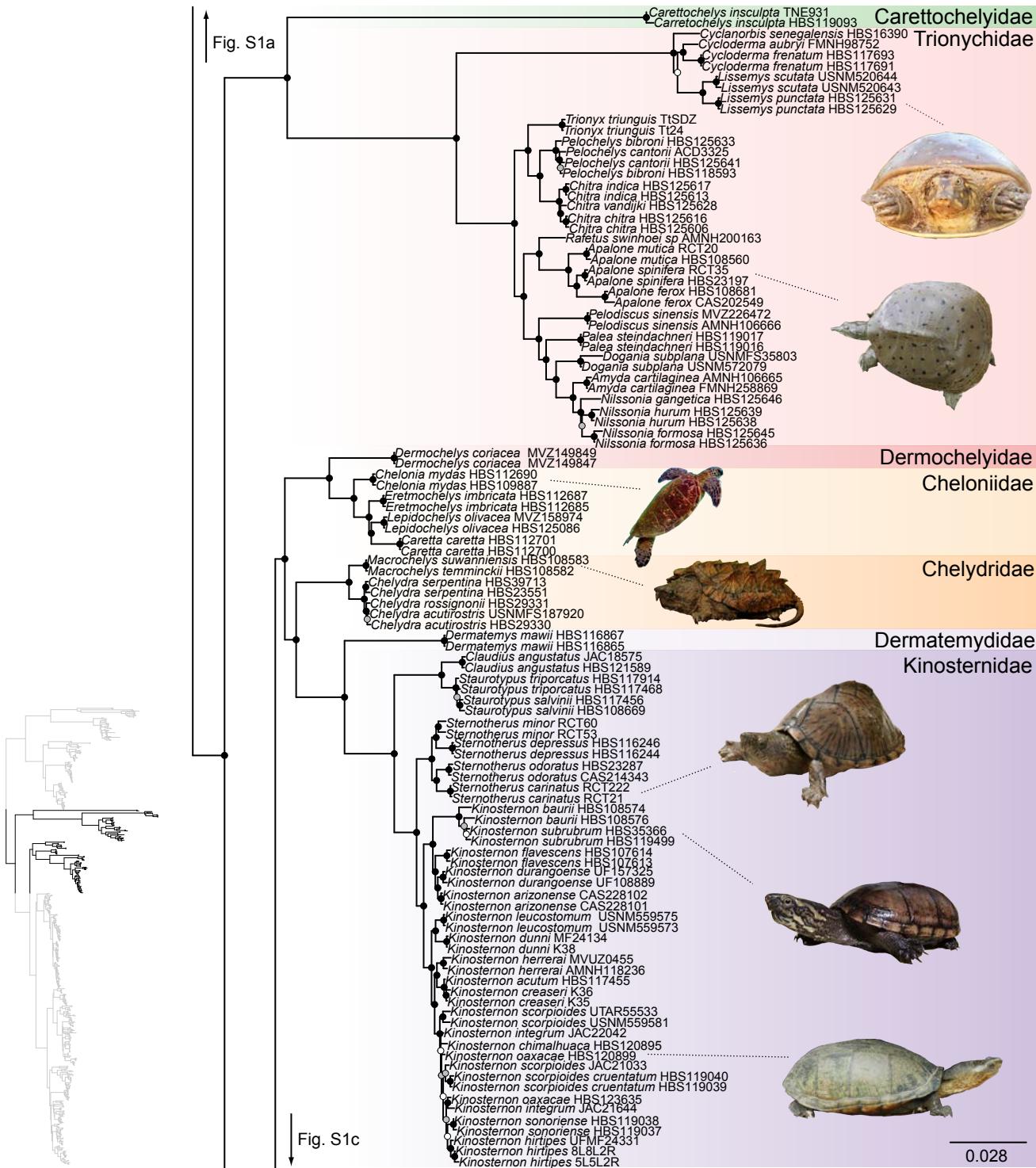
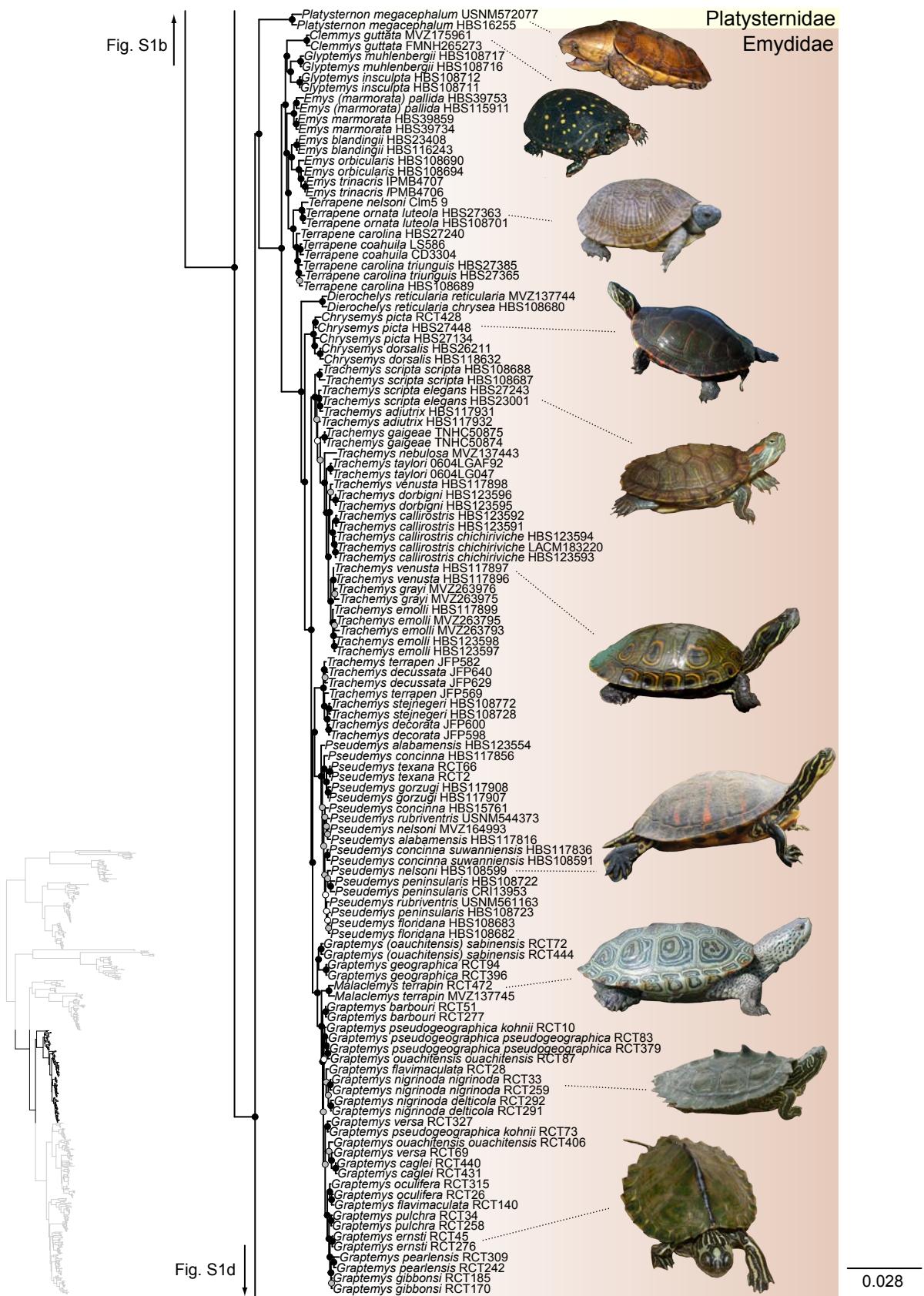
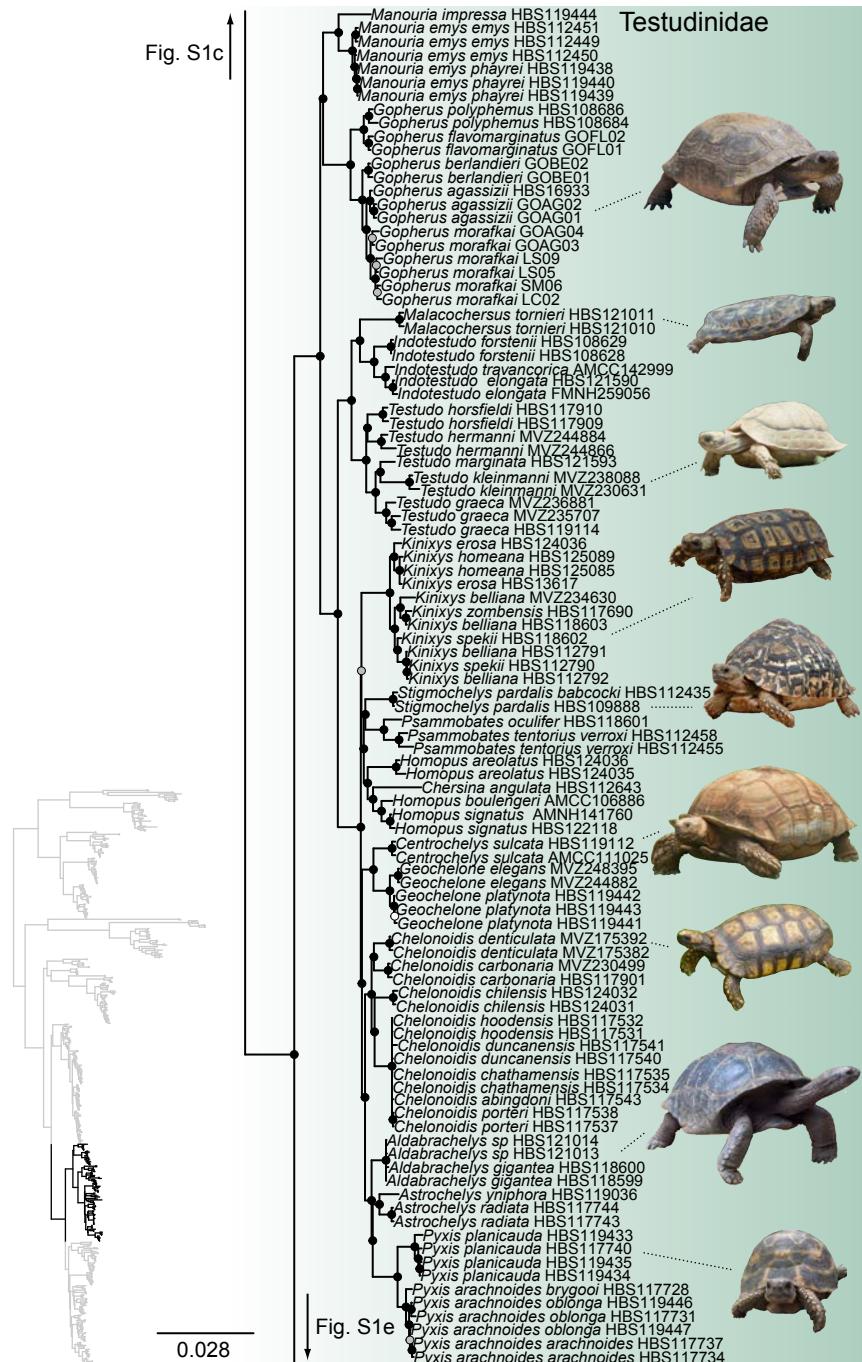
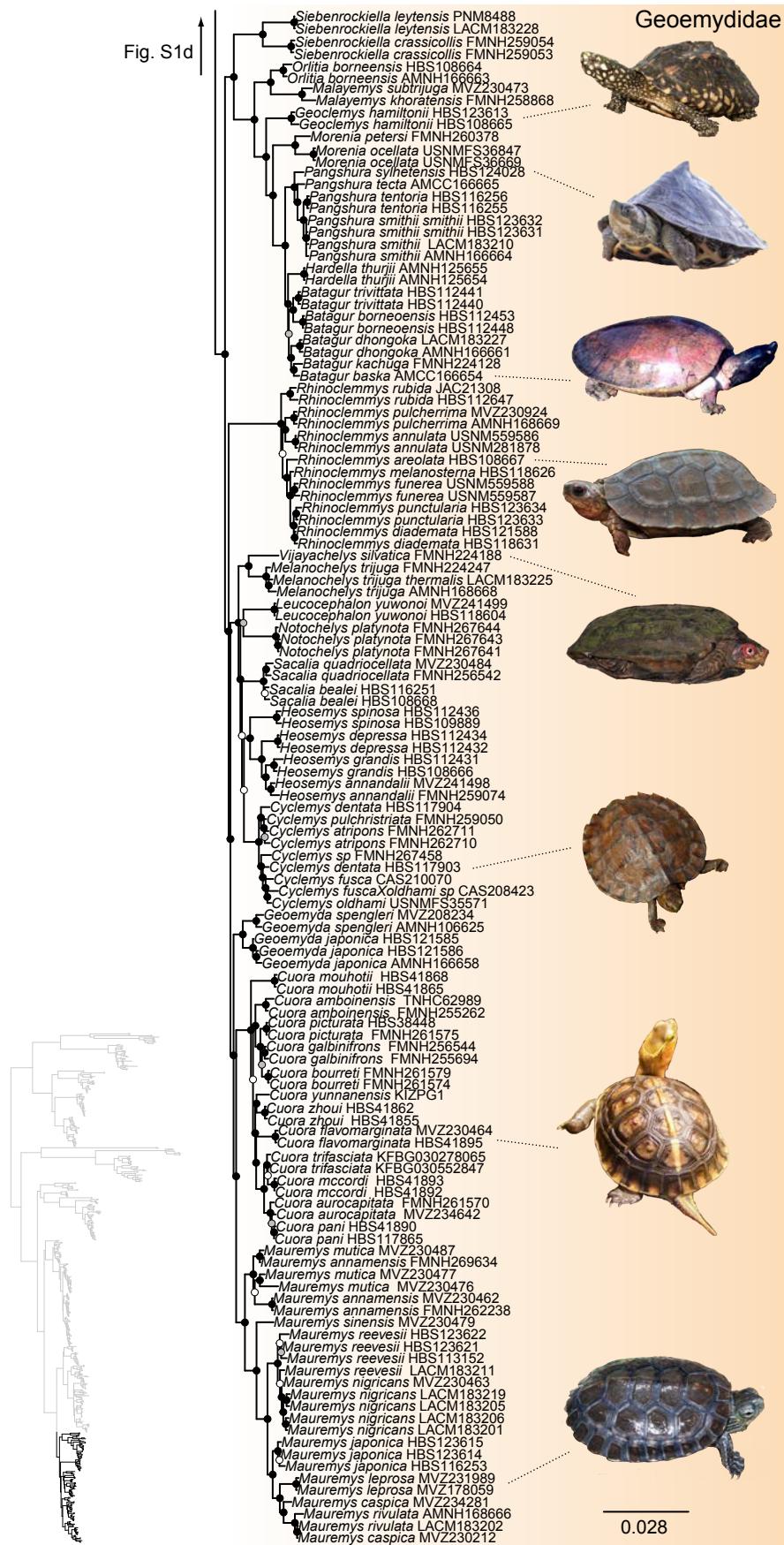


Fig. S1b









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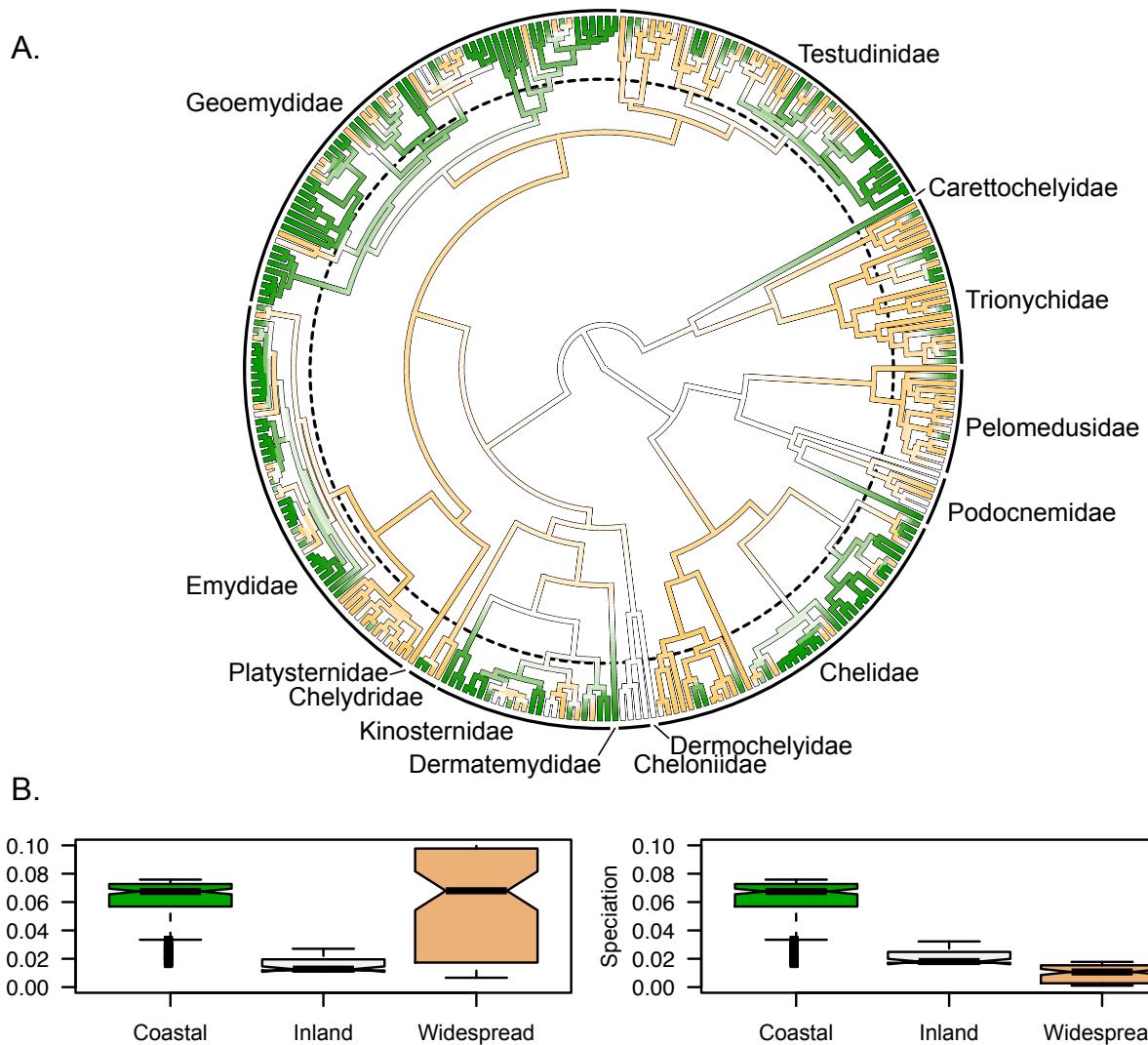


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